

FIGURE 1A

[illegible]

FIGURE 1B

1201	E N V V E M Y N S Y L V G D E L W V V M E F L E G	400
	GGCGCCCTCACCGACATCGTCACCCACACAGGATGAACGAGGAGCAGATCGCGCGCGTGTGCCTTGCAGTGTG	
425	G A L T D I V T H T R M N E E O I A A V C L A V L	
1276	CAGGCCCTGTCGGTGTCTCCACGCCCGAGGGCGTCATCCACGGGACATCAAGAGCGACTCGATCCTGCTGACCCCAT	
450	O A L S V L H A O G V I H R D I K S D S I L L T H	
1351	GATGGCAGGTGAAGCTGTCAGACTTTGGGTTCTGCGCCCGAGGTGAGCAAGGAAGTCCCCGAAGGAGTCGCTG	
475	D G R V K L S D F G F C A O V S K E V P R R K S L	
1426	GTCGGCACGCCCTACTGGATGGCCCCCAGAGCTCATCTCCCGCCTTCCCTACGGGCCAGAGGTAGACATCTGGTCG	
500	V G T P Y W M A P E L I S R L P Y G P E V D I W S	
1501	CTGGGGATAATGGTGATTGAGATGGTGACGGAGAGCCCCCTACTTCAACGAGGCCACCCCTCAAAGCCATGAAG	
525	L G I M V I E M V D G E P P Y F N E P P L K A M K	
1576	ATGATTCGGGACAAACCTGCCACCCCGACTGAAGAACCCTGCACAAGGTGTGCGCATCCCTGAAGGGCTTCCTGGAC	
550	M I R D N L P P R L K N L H K V S P S L K G F L D	
1651	CGCCTGCTGGTGCAGACCCCTGCCCGAGCGGGCCACGGCAGCCGAGCTGCTGAAGCACCCCATTCCTGGCCAAAGGCA	
575	R L L V R D P A O R A T A A E L L K H P F L A K A	
1726	GGGCCGCTGCCAGCATCGTGTCCCTCAATGCGCCAGAACCGCACCATGA	
591	G P P A S I V P L M R Q N R T R *	

FIGURE 1C

PAK4 PAK2 SITE20	324 251 623	I										II										III										Vla									
		FIKIGEGSTGIVCIATVVRSSGKLVAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY									
		YEKIGQGASGTVFTATDVALLGQEVATIKQINLQKQPKKELIINEILVMMKEL										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY									
PAK4 PAK2 SITE20	374 301 674	IV										V										Vla										Vla									
		QHENVVEMYN SYLVGDELWVVMEEFL EGGALTDI VTHTRMNEE QIAAVCLA										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY									
		KNPNI VNF L DSYLVGDEL FVVM EYLL AGRSLTDVVTETCTMDEA QIAAVCRE										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY									
PAK4 PAK2 SITE20	424 351 724	VIIb										VII										VII										VII									
		VLQALSVLHAQQGV IHRDIKSDSILL THDGRVKLSDFGFCAQVSK EVPRRK										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY									
		CLQALEFLHANQV IHRDIKSDNVLL GMEGSSVKLTDFGFCAQITP EQSKRS										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY									
PAK4 PAK2 SITE20	474 401 774	VIII										IX										IX										IX									
		SLVGTPTYWMAPELI SRLPYGPEVDIWSL GIMV IEMVDGEPPY ENEPPLKA										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY									
		TMVGTPTYWMAPEVV TRKAYGPKVDIWSL GIMV IEMVGEPPY ENEPPLRA										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY									
PAK4 PAK2 SITE20	524 451 824	X										XI										XI										XI									
		MKMITRKNLPRLKNLHKVSPSLKGFLLDRLLVRDPQAQRATA AELLKHPFLA										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY									
		LYLIATNGTPELQMPENLSP IFRDFFLNRCLEMDV EKRGS A KELLQHPFLK										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY									
PAK4 PAK2 SITE20	524 451 824	X										XI										XI										XI									
		LYLIATNGTPELQMPENLSP IFRDFFLNRCLEMDV EKRGS A KELLQHPFLK										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY									
		LYLIATNGTPELQMPENLSP IFRDFFLNRCLEMDV EKRGS A KELLQHPFLK										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY										VAVK KMDLRRKQQRREL LFNENEVVI MRDY									

FIGURE 1D

PAK4	10	EISAPSNFEH	R	V	H	T	G	F	D	Q	H	E	Q	30
PAK2	71	EISPPSD	F	E	H	T	I	H	V	G	F	D	A	91
STE20	317	ISYNA	--	K	H	I	H	V	G	V	D	S	K	362
WASP	238	DIGAPSG	F	K	H	V	S	H	V	G	W	D	P	258
CLA4	183	GVSSPTN	F	T	H	K	V	H	V	G	F	D	P	203

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FIGURE 1E

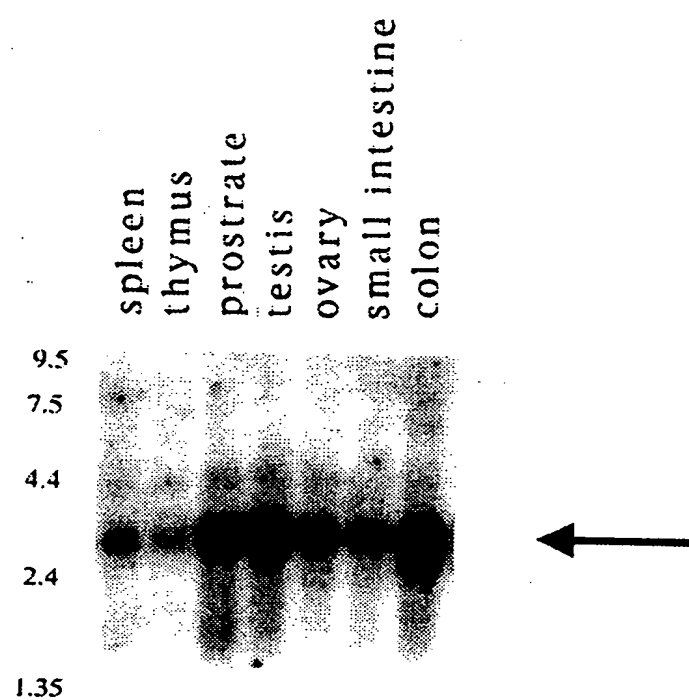


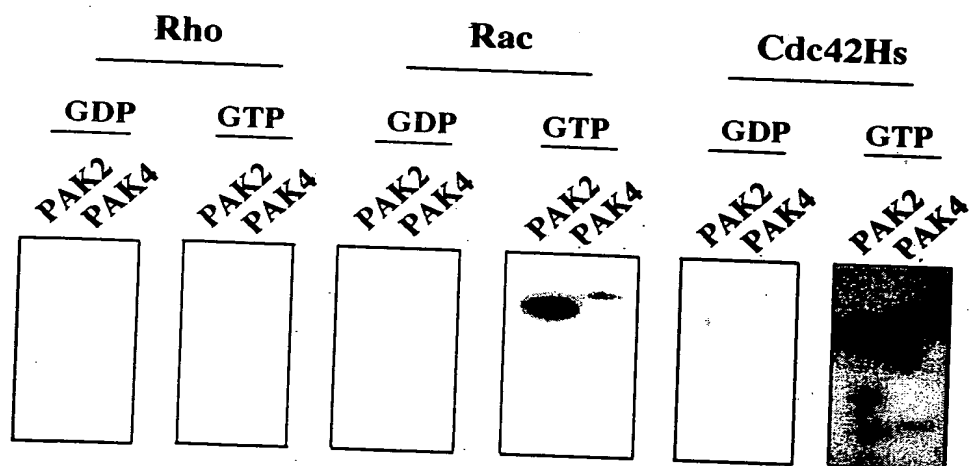
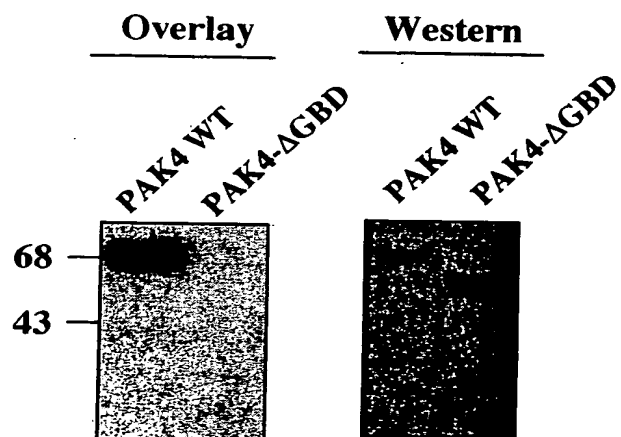
FIGURE 2A**FIGURE 2B**

FIGURE 3A

A.

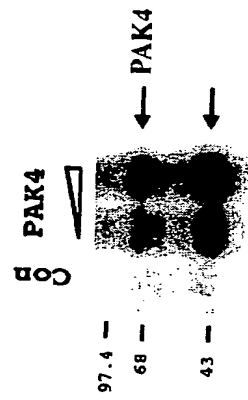


FIGURE 3B

B.



FIGURE 3C

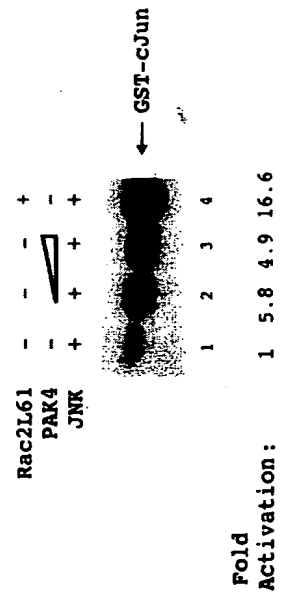


FIGURE 3D

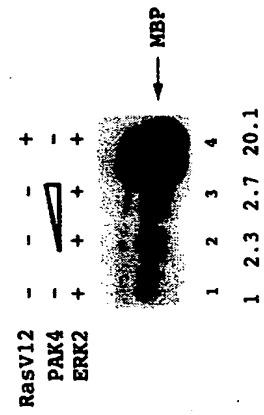


FIGURE 3E

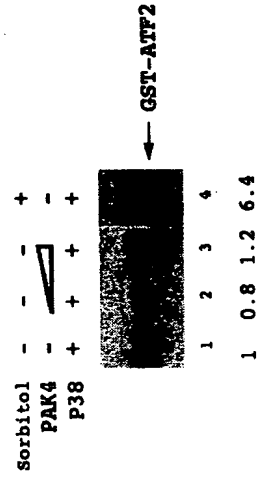


FIGURE 4B
Actin

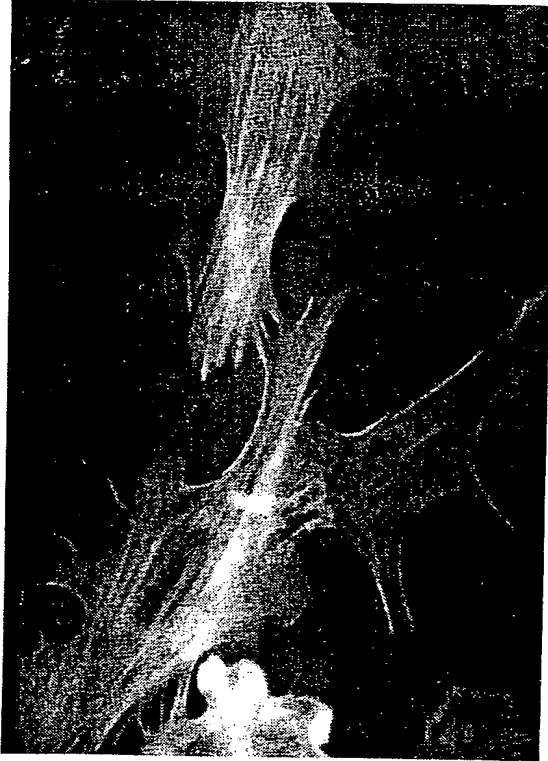


FIGURE 4A
Anti-HA



PAK4

FIGURE 4D

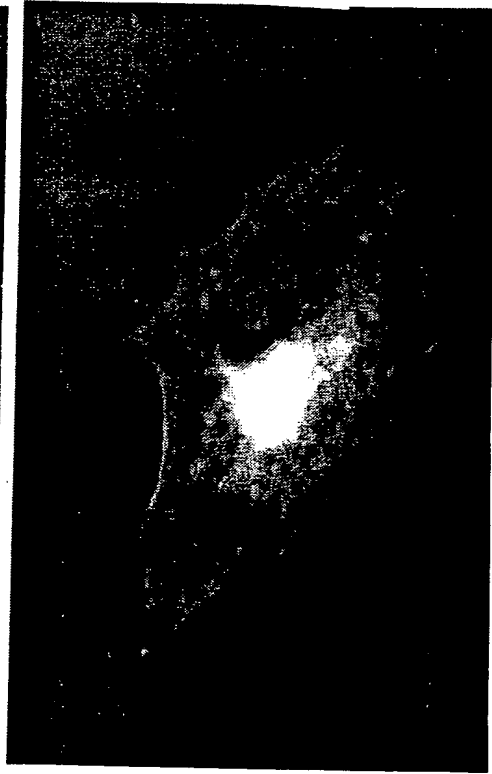
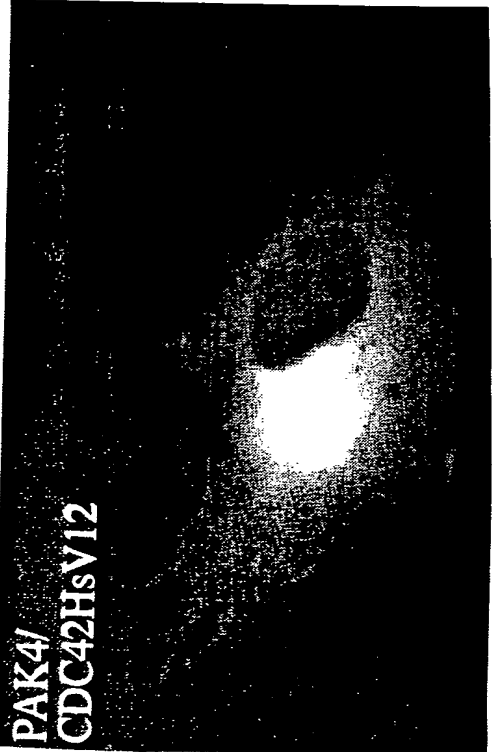


FIGURE 4C



**PAK4/
CDC42HsV12**

FIGURE 4E

Anti-HA

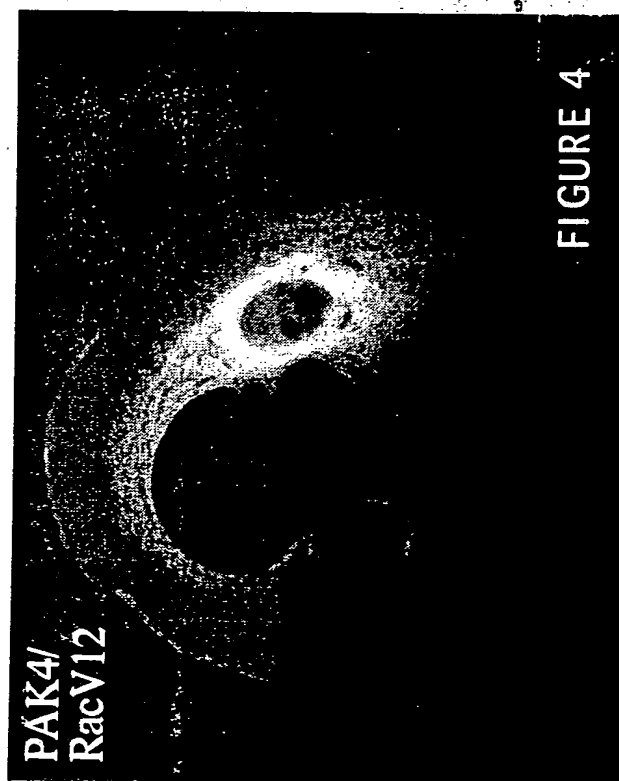


FIGURE 4F

Actin



FIGURE 4H

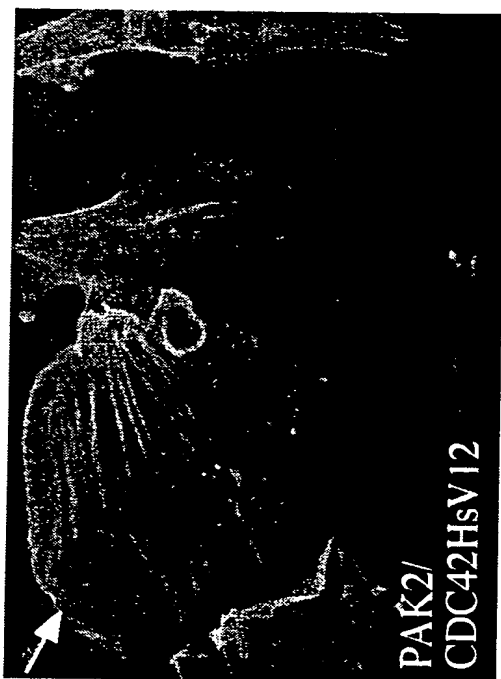


FIGURE 4G

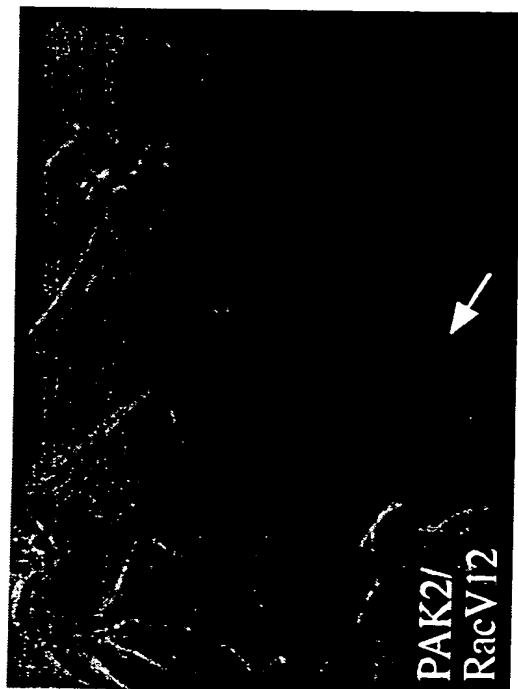


FIGURE 4J

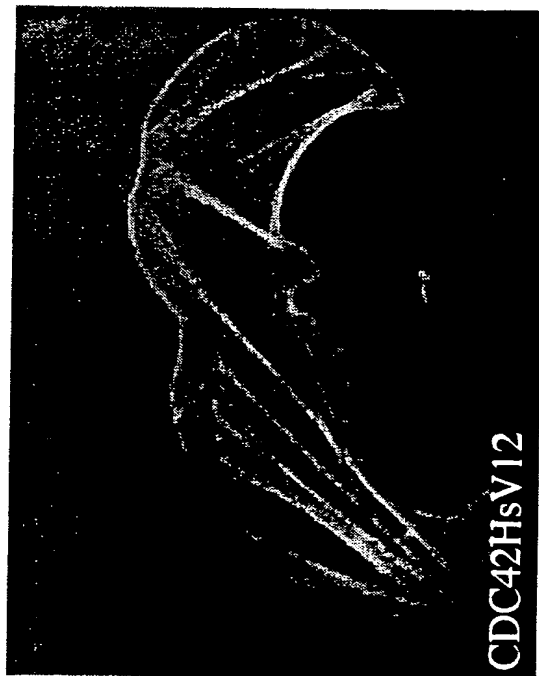


FIGURE 4I

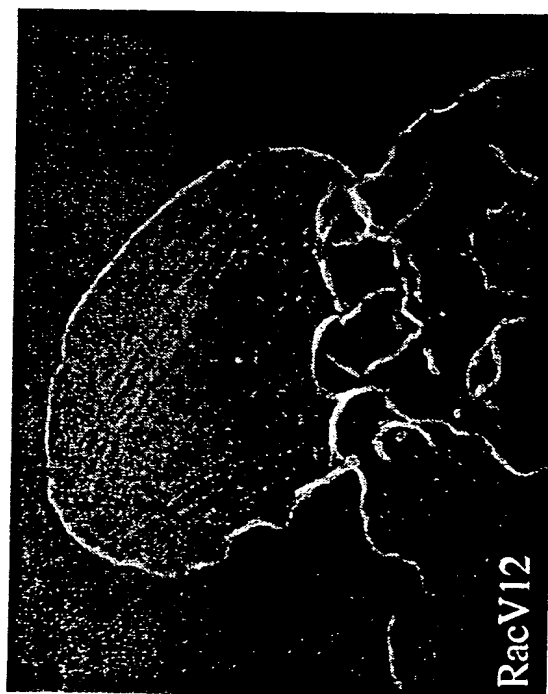


FIGURE 5A

Anti-HA



FIGURE 5B

Anti- β -COP

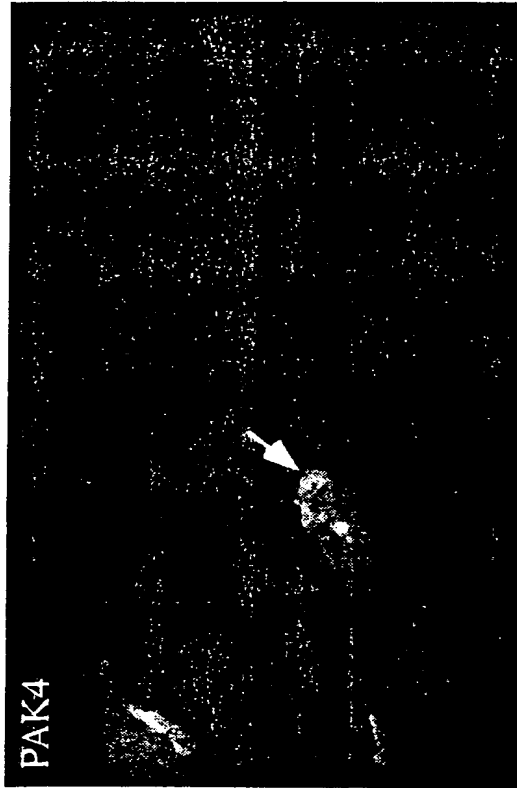


FIGURE 5C

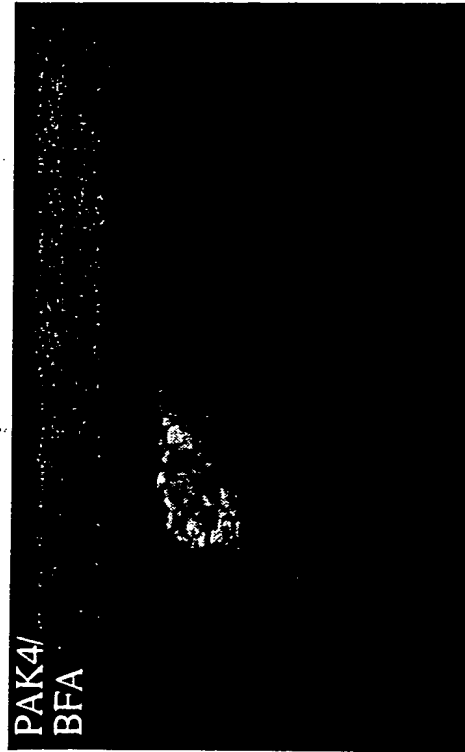


FIGURE 5D

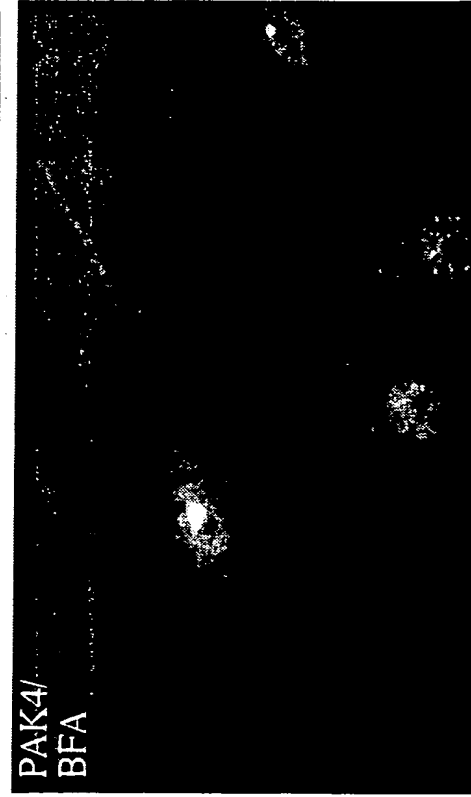


FIGURE 5E
Anti- β -COP

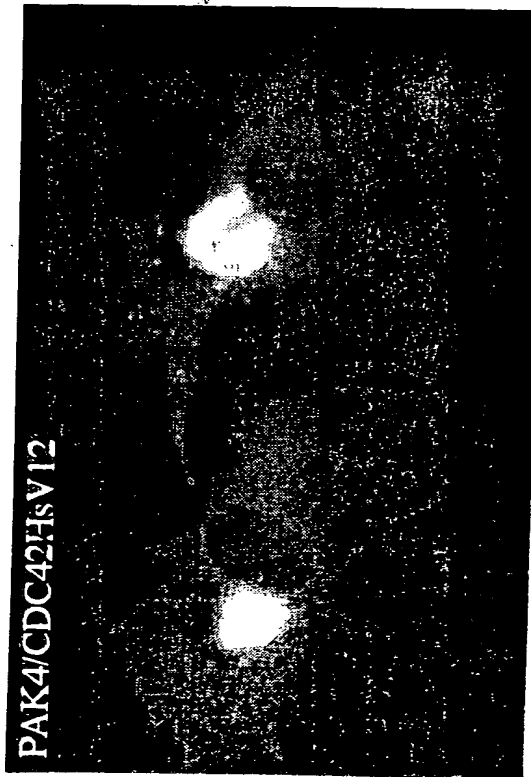


FIGURE 5F
Anti-HA

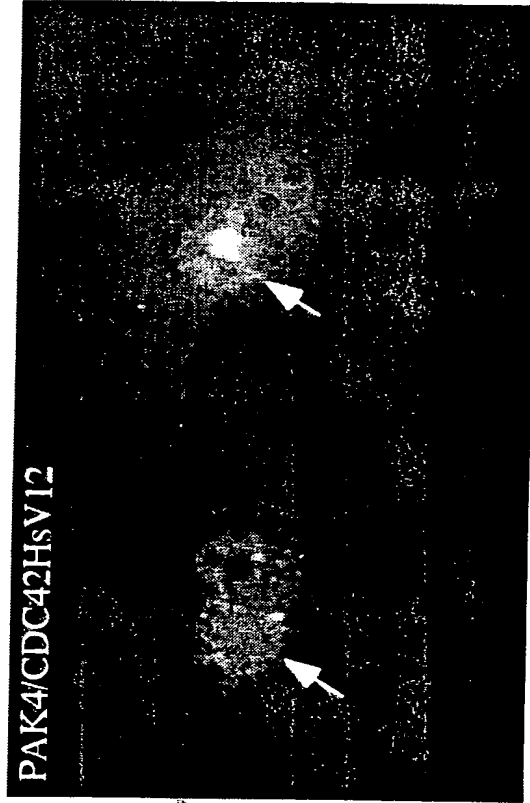


FIGURE 5G

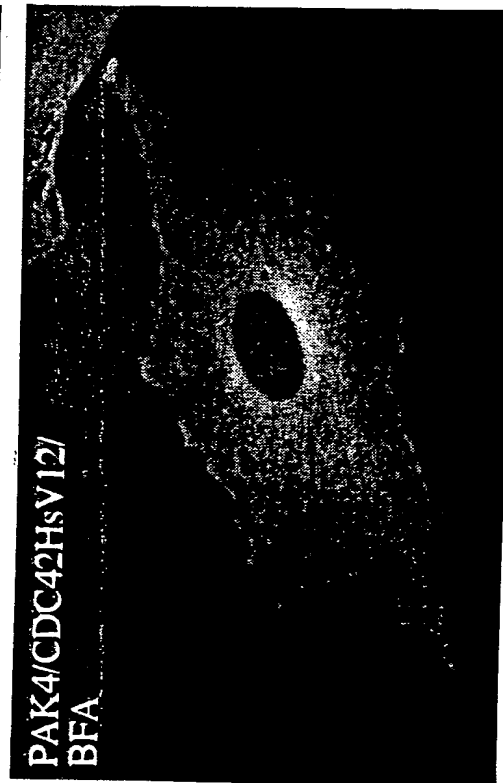


FIGURE 5H

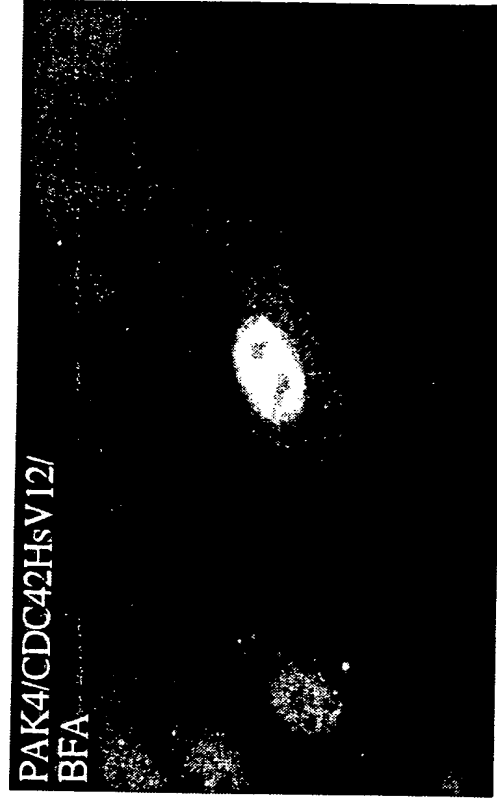


FIGURE 6A

Anti-HA

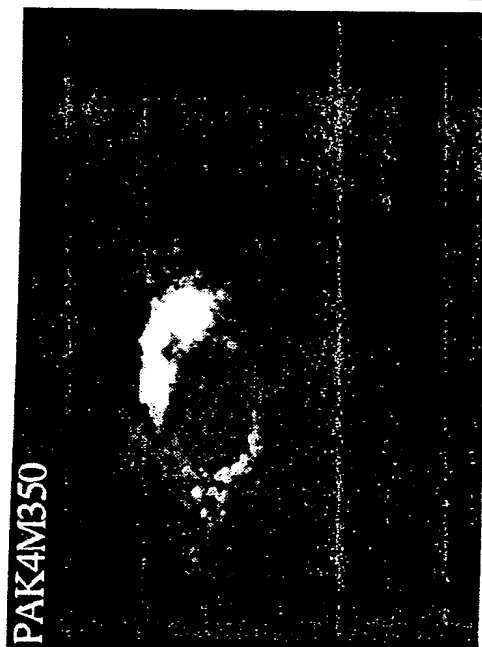
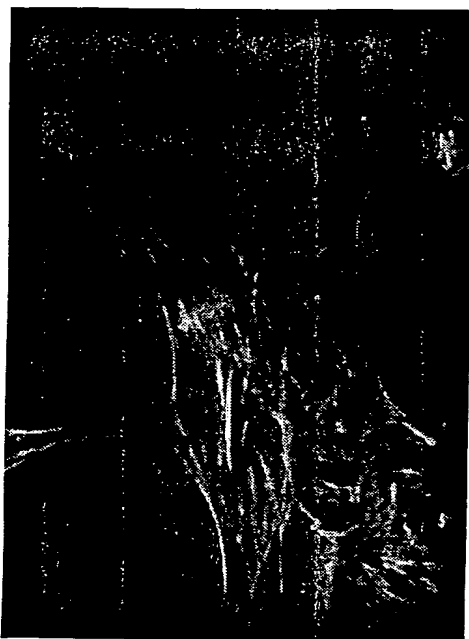


FIGURE 6B

Anti- β -COP



PAK4M350/
CDC42HsV12

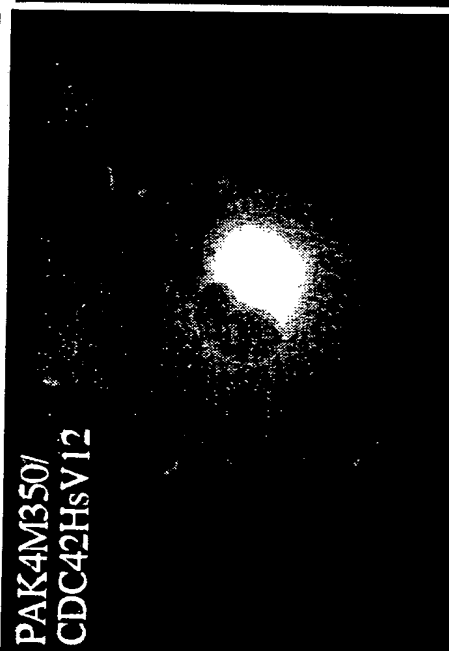


FIGURE 6C

FIGURE 6D

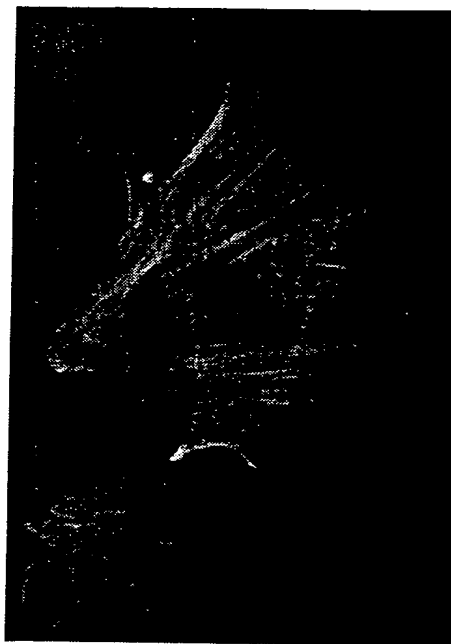


FIGURE 6E

Anti-HA



FIGURE 6F

Actin

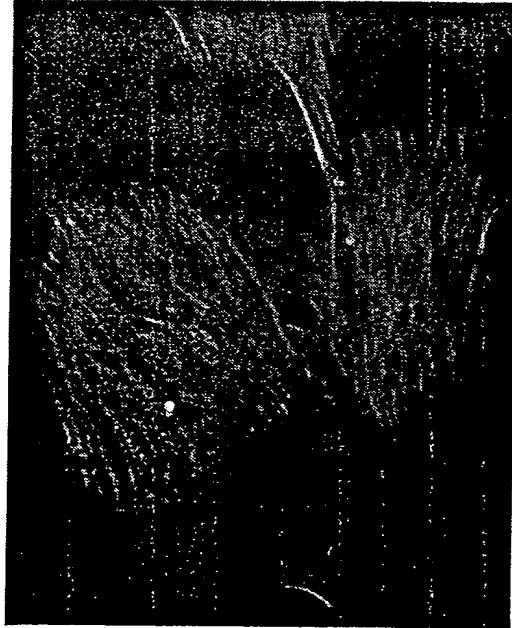


FIGURE 6G



FIGURE 6H

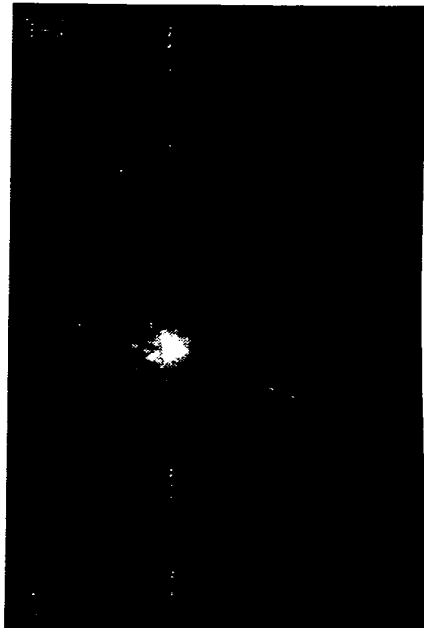
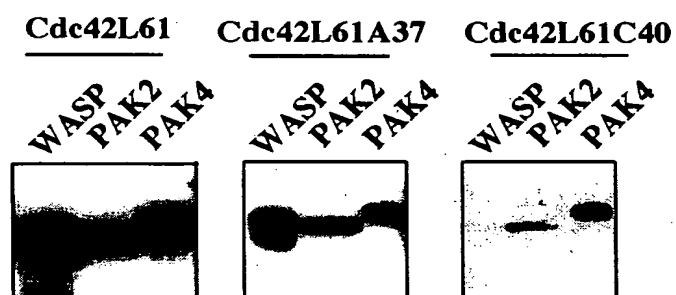


FIGURE 7A

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FIGURE 7B

Anti-HA

PAK4 + Cdc42L61C40

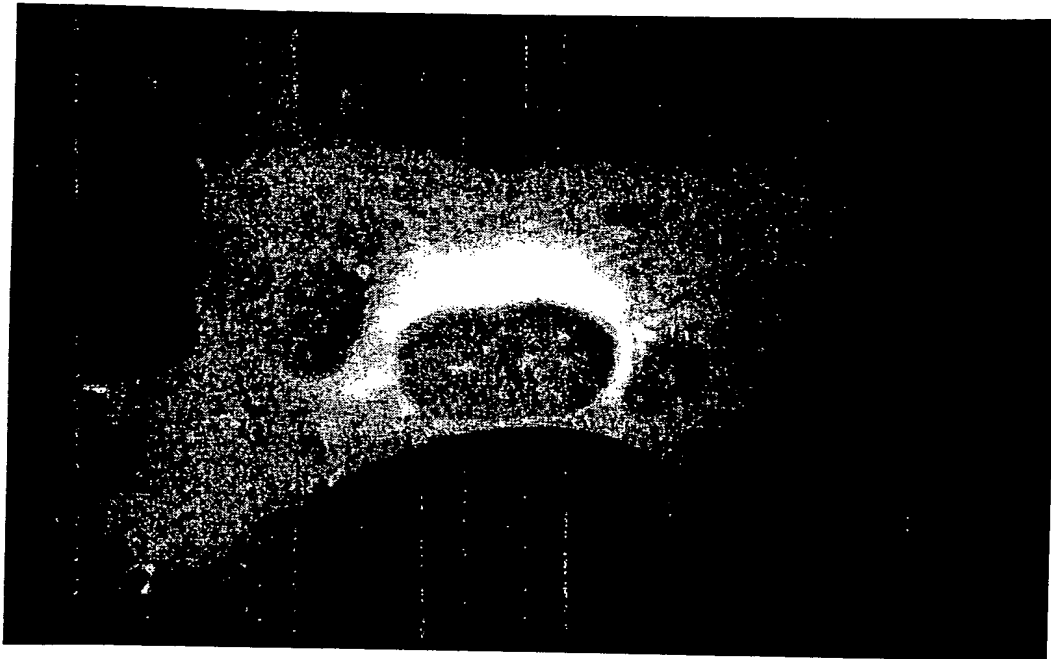


FIGURE 7C

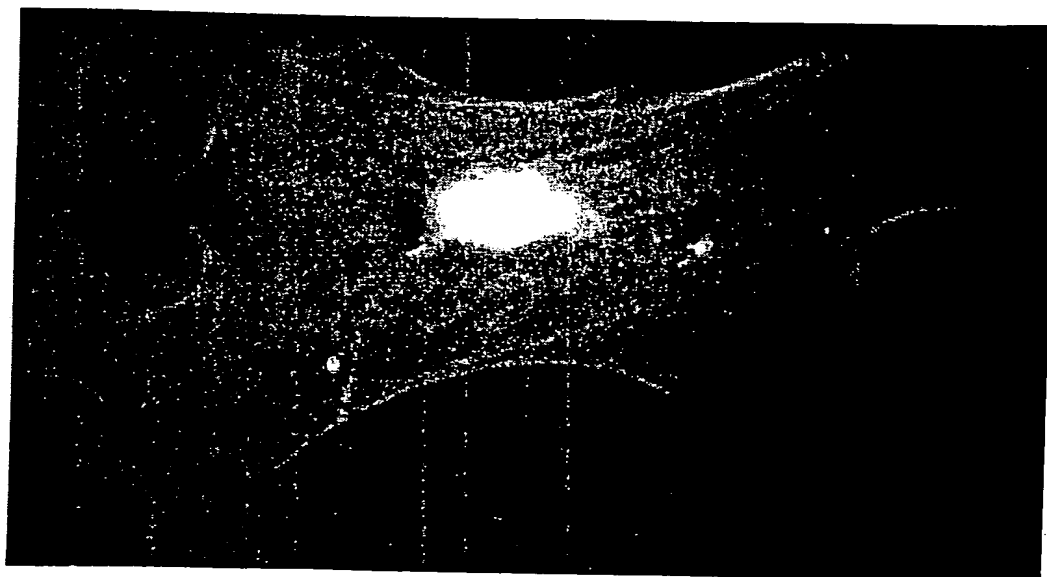


FIGURE 8A

Partial cDNA of the mouse PAK4:

AAGCAGCAGC GGGCGAGTT GCTCTTCAAT GAGGTGGTGA TCATGCGGGA
 CTACCGGCAC GAGAACGTGG TGGAGATGTA CAACAGCTAC CTGGTGGGTG
 ACGAACTCTG GGTGTCATG GAGTTCTTG AAGCGGCGC CCTCACGGAT
 ATTGTCACCC ACACCAGGAT GAACGAGGAA CAGATCGCCG CCGTGTGCCCT
 GGCTGTGCTT CAGGCGCTGG CTGTGCTCCA CGCCAGGGT GTCATCCACA
 GCGACATAAA AACGGACA

predicted amino acid sequence of the partial mouse PAK4 cDNA:

FIGURE 8B

KQQRRELLFN EVVMRDYRHN EVVMYNSY LVGDELWVVM EFLEGGALTD
 IVTHTRMNEEQIAA VCLAVLQALAVLHAQG VIHSDIKTD

Partial genomic sequence of mouse PAK4:

FIGURE 8C

ACCTGGTGGG TGACGAACCTCTGGGTGGTCA TGGAGTTCCT GGAAGGCGGC
 GCCCTCACGG ATATTGTCAC CCACACCAGG T'ACCAI'AGGG CAGCCTGCTG
 GCTCATGTGC TCCCTGGGGT GGAACTGGGA CCCTTTAGGC TCTGGTGATA
 GACAAGTGCC CTCCAGAGTG TGGGTGGGGC AGTGAGGCCA GGCACACAGG
 ATGGGGGTCA TAGCATCGTG GCTCCCTGAC CCCGTGTTGAG GCGGGTCTTT
 GTGACCTCTT GTTGTCTAAA GCAGGGTAGG GGCCTCTTCA CTGCCCACTC
 TACCCCCAGG GTGGGATGCC CAAGGCAGCG CTGAGTGCCC AGTTGCTCCT
 CTGCCCGCGC AGGATGAACG AGGAACAGAT CCGCGCCCGT GTGCCCTGGCT
 TGTGCTTCAN GCGCTGGCTT GTGCTCCACG CCCAGGGTGT CATCCACCGT
 GACATCAAGA GTGACTCTAT CTGCTGACCCATGATGGC